Rec'd PCT/PTO   2 0 AUG 2004

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RAW SEQUENCE LISTING              DATE: 08/26/2004
PATENT APPLICATION:  US/10/505,145   TIME: 11:31:53

Input Set : A:\56159-5241 Sequence Listing.txt
Output Set: N:\CRF4\08262004\J505145.raw
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     3 <110> APPLICANT: COLLIVER, Steven Peter
     4        DOBB, Roy Thomas
     5        van der HIJDEN, Hendrikus Theodorus Wilhelmus Maria
     7 <120> TITLE OF INVENTION: PRODUCTION OF DADZEIN IN TRANSGENIC PLANTS
     9 <130> FILE REFERENCE: 56159-5241
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/505,145
C--> 11 <141> CURRENT FILING DATE: 2004-08-20
    11 <150> PRIOR APPLICATION NUMBER: PCT/EP03/01465
    12 <151> PRIOR FILING DATE: 2003-02-13
    14 <150> PRIOR APPLICATION NUMBER: EP 02251404.6
    15 <151> PRIOR FILING DATE: 2002-02-28
    17 <160> NUMBER OF SEQ ID NOS: 59
    19 <170> SOFTWARE: PatentIn version 3.2
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    22 <211> LENGTH: 946
    23 <212> TYPE: DNA
    24 <213> ORGANISM: Pisum sativum
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    29 cctgttgttg gaatgggatc agcacctgac ttcacatgca agaaagacac taaagaagca     120
    31 atcatcgaag ccatcaaaca aggttacaga cactttgata ctgctgctgc ttatggatcc     180
    33 gaacaagctc ttggtgaggc tttgaatgag gctattcaac ttggtcttgt cactagagaa     240
    35 cagctttttg ttacttctaa actttgggtt actgaaaatc atcctcacct tgttcttcct     300
    37 gctctacaaa aatctctcaa gactcttcag ttggattact tggatttgta tttgattcat     360
    39 tggccactta gttctcagcc cggaaagttt tcatttccaa ttgatgtggc tgatctattg     420
    41 ccatttgatg taaaaggtgt gtgggaatcc atggaagagg ctttgagact tggactcacg     480
    43 aaagctattg gtgtcagtaa cttctctgtc aagaaacttc aaaagctact atctgttgcc     540
    45 actgttcttc ctgctgttaa tcaagtagag atgaaccttg catggcaaca aaagaagcta     600
    47 agagaatttt gcaatgaaaa tggaatagtg ttgactgcat tttcaccgtt gaggaaaggc     660
    49 gccagccgag gagcaaatga ggttatggag aatgatatgc ttaaacagat tgcagatgct     720
    51 catggaaagt ctattgcaca aatttctctg agatggttat atgaacaagg aatcactttt     780
    53 gttccaaaga gctatgataa ggagagaatg agtcaaaatt tgagaatctt tgattggaca     840
    55 ctgacaaagg aggatcatga gaaaattgat caaattaagc agaatcgttt gatccctgga     900
    57 ccaaccaagc caagtctcaa tgatctttgg gatgatgaaa tataag              946
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    61 <211> LENGTH: 314
    62 <212> TYPE: PRT
    63 <213> ORGANISM: Pisum sativum
    65 <400> SEQUENCE: 2
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    68 1               5                   10                  15
    71 Gln Ile Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
    72              20                  25                  30
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76      35              40              45
79  Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
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83  Gly Glu Ala Leu Asn Glu Ala Ile Gln Leu Gly Leu Val Thr Arg Glu
84  65              70              75              80
87  Gln Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
88              85              90              95
91  Leu Val Leu Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Asp
92              100             105             110
95  Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
96      115             120             125
99  Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
100     130             135             140
103 Lys Gly Val Trp Glu Ser Met Glu Glu Ala Leu Arg Leu Gly Leu Thr
104 145             150             155             160
107 Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Lys Leu
108             165             170             175
111 Leu Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn
112             180             185             190
115 Leu Ala Trp Gln Gln Lys Lys Leu Arg Glu Phe Cys Asn Glu Asn Gly
116     195             200             205
119 Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly Ala Ser Arg Gly
120     210             215             220
123 Ala Asn Glu Val Met Glu Asn Asp Met Leu Lys Gln Ile Ala Asp Ala
124 225             230             235             240
127 His Gly Lys Ser Ile Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln
128             245             250             255
131 Gly Ile Thr Phe Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Ser Gln
132             260             265             270
135 Asn Leu Arg Ile Phe Asp Trp Thr Leu Thr Lys Glu Asp His Glu Lys
136             275             280             285
139 Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly Pro Thr Lys Pro
140     290             295             300
143 Ser Leu Asn Asp Leu Trp Asp Asp Glu Ile
144 305             310
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 1567
149 <212> TYPE: DNA
150 <213> ORGANISM: Glycine max
152 <400> SEQUENCE: 3
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155 acacccactg caaaatcaaa agcacttcgc catctcccaa acccaccaag cccaaagcct     120
157 cgtcttccct tcataggaca ccttcatctc ttaaaagaca aacttctcca ctacgcactc     180
159 atcgacctct ccaaaaaaca tggtcccttca ttctctctct actttggctc catgccaacc     240
161 gttgttgcct ccacaccaga attgttcaag ctcttcctcc aaacgcacga ggcaacttcc     300
163 ttcaacacaa ggttccaaac ctcagccata agacgcctca cctatgatag ctcagtggca     360
165 atggttccct tcgggcccta ctggaagttc gtgaggaagc tcatcatgaa cgaccttctc     420
167 aacgccacca ctgtaaacaa gttgaggcct ttgaggaccc aacagacgcg taagttcctt     480
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169 agggttatgg cccaaggcgc agaggcacag aagccccttg acttgaccga ggagcttctg   540
171 aaatggacca acagcaccat ctccatgatg atgctcggcg aggctgagga gatcagagac   600
173 atcgctcgcg aggttcttaa gatctttggc gaatacagcc tcactgactt catctggcca   660
175 ttgaagcatc tcaaggttgg aaagtatgag aagaggatcg acgacatctt gaacaagttc   720
177 gaccctgtcg ttgaaagggt catcaagaag cgccgtgaga tcgtgaggag gagaaagaac   780
179 ggagaggttg ttgagggtga ggtcagcggg gttttccttg acactttgct cgagttcgct   840
181 gaggatgaga ctatggagat caaaatcacc aaggaccaca tcaagggtct tgttgtagac   900
183 ttttctcgg caggaacaga ctcaacagcg gtggcaacag agtgggcatt ggcagaactc   960
185 atcaacaatc ctaaggtgtt ggaaaaggct cgtgaggagg tctacagtgt tgtgggaaag  1020
187 gacagacttg tggacgaagt tgacactcaa aaccttcctt acattagagc aatcgtgaag  1080
189 gagacattcc gcatgcaccc gccactccca gtggtcaaaa gaaagtgcac agaagagtgt  1140
191 gagattaatg gatatgtgat cccagaggga gcattgattc tcttcaatgt atggcaagta  1200
193 ggaagagacc ccaaatactg ggacagacca tcggagttcc gtcctgagag gttcctagag  1260
195 acaggggctg aaggggaagc agggcctctt gatcttaggg gacaacattt tcaacttctc  1320
197 ccatttgggt ctgggaggag aatgtgccct ggagtcaatc tggctacttc gggaatggca  1380
199 acacttcttg catctcttat tcagtgcttc gacttgcaag tgctgggtcc acaaggacag  1440
201 atattgaagg gtggtgacgc caaagttagc atggaagaga gagccggcct cactgttcca  1500
203 agggcacata gtcttgtctg tgttccactt gcaaggatcg gcgttgcatc taaactcctt  1560
205 tcttaag                                                           1567
208 <210> SEQ ID NO: 4
209 <211> LENGTH: 521
210 <212> TYPE: PRT
211 <213> ORGANISM: Glycine max
213 <400> SEQUENCE: 4
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219 His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
220             20                  25                  30
223 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
224         35                  40                  45
227 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
228     50                  55                  60
231 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
232 65                  70                  75                  80
235 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
236             85                  90                  95
239 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
240             100                 105                 110
243 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
244         115                 120                 125
247 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
248     130                 135                 140
251 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
252 145                 150                 155                 160
255 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
256             165                 170                 175
259 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
260             180                 185                 190
263 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
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264         195                  200                  205
267 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
268     210                  215                  220
271 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
272 225                  230                  235                  240
275 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
276                  245                  250                  255
279 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
280                  260                  265                  270
283 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
284         275                  280                  285
287 Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
288         290                  295                  300
291 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
292 305                  310                  315                  320
295 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
296                  325                  330                  335
299 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
300             340                  345                  350
303 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
304         355                  360                  365
307 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
308         370                  375                  380
311 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
312 385                  390                  395                  400
315 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
316                  405                  410                  415
319 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
320         420                  425                  430
323 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
324         435                  440                  445
327 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
328     450                  455                  460
331 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
332 465                  470                  475                  480
335 Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
336                  485                  490                  495
339 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
340             500                  505                  510
343 Ile Gly Val Ala Ser Lys Leu Leu Ser
344         515                  520
347 <210> SEQ ID NO: 5
348 <211> LENGTH: 670
349 <212> TYPE: DNA
350 <213> ORGANISM: Lotus corniculatus
352 <400> SEQUENCE: 5
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355 tctccagcca ccgccaagtc ttatttcctc ggtggtgcag gggagagagg gttgacgatt   120
357 gaggggaagt tcataaaatt cactggcata ggagtgtatt tggaagatac agcagtggat   180
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359  tcactcgcca  ccaagtggaa  gggtaagagt  tcacaagagc  tgcaggactc  ccttgacttc   240
361  ttcagagaca  tcatttcaag  tccctctgag  aagttaattc  gagggtccaa  gctgaggcca   300
363  ttgagtggcg  tggagtattc  aagaaaggtg  atggagaatt  gtgtggcaca  catgaagtct   360
365  gctggaactt  atggtgaagc  agaggccaca  gccattgaaa  aatttgcaga  agccttcagg   420
367  aaggtggatt  ttccaccagg  ttcctctgtt  ttctaccgac  aatcaacaga  tggaaaatta   480
369  gggcttagtt  tctctttgga  tgacacgata  ccagaagaag  aggctgtagt  tatagagaac   540
371  aaggcactct  cagaggcagt  gttagagacc  atgattggcg  agcatgctgt  ttcccctgat   600
373  ttgaagcgtt  gtttggctga  aaggttgcct  attgtgatga  accagggtct  tctcctcact   660
375  ggaaactgat                                                              670
378  <210> SEQ ID NO: 6
379  <211> LENGTH: 222
380  <212> TYPE: PRT
381  <213> ORGANISM: Lotus corniculatus
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390              20                  25                  30
393  Ala Gly Glu Arg Gly Leu Thr Ile Glu Gly Lys Phe Ile Lys Phe Thr
394          35                  40                  45
397  Gly Ile Gly Val Tyr Leu Glu Asp Thr Ala Val Asp Ser Leu Ala Thr
398      50                  55                  60
401  Lys Trp Lys Gly Lys Ser Ser Gln Glu Leu Gln Asp Ser Leu Asp Phe
402  65                  70                  75                  80
405  Phe Arg Asp Ile Ile Ser Ser Pro Ser Glu Lys Leu Ile Arg Gly Ser
406                  85                  90                  95
409  Lys Leu Arg Pro Leu Ser Gly Val Glu Tyr Ser Arg Lys Val Met Glu
410                  100                 105                 110
413  Asn Cys Val Ala His Met Lys Ser Ala Gly Thr Tyr Gly Glu Ala Glu
414              115                 120                 125
417  Ala Thr Ala Ile Glu Lys Phe Ala Glu Ala Phe Arg Lys Val Asp Phe
418      130                 135                 140
421  Pro Pro Gly Ser Ser Val Phe Tyr Arg Gln Ser Thr Asp Gly Lys Leu
422  145                 150                 155                 160
425  Gly Leu Ser Phe Ser Leu Asp Asp Thr Ile Pro Glu Glu Glu Ala Val
426                  165                 170                 175
429  Val Ile Glu Asn Lys Ala Leu Ser Glu Ala Val Leu Glu Thr Met Ile
430              180                 185                 190
433  Gly Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Glu Arg
434              195                 200                 205
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438      210                 215                 220
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442  <211> LENGTH: 9
443  <212> TYPE: PRT
444  <213> ORGANISM: Artificial Sequence
446  <220> FEATURE:
447  <223> OTHER INFORMATION: Description of Artificial Sequence:conserved
448        regions of various known CHR's
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VERIFICATION SUMMARY   DATE: 08/26/2004
PATENT APPLICATION: **US/10/505,145**   TIME: 11:31:54

Input Set : **A:\56159-5241 Sequence Listing.txt**
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date